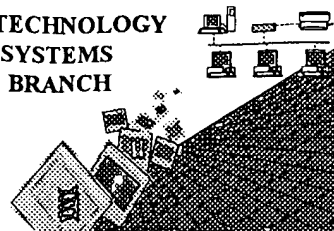


BIOTECHNOLOGY  
SYSTEMS  
BRANCH



RAW SEQUENCE LISTING  
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/087,782  
Source: OLPE  
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FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

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Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

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2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:  
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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/087,782

DATE: 03/20/2002

TIME: 16:25:09

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Output Set: N:\CRF3\03202002\J087782.raw

*pg 1,5*  
Does Not Comply  
Corrected Diskette Needed

3 <110> APPLICANT: AVENTIS PHARMA SA  
4 US GOVERNMENT of the UNITED STATES  
6 <120> TITLE OF INVENTION: NUCLEIC ACID OF THE HUMAN ABCC11 GENE, VECTORS  
7 CONTAINING SUCH NUCLEIC ACID, AND USES THEREOF  
9 <130> FILE REFERENCE: ABCC11 GENE  
11 <140> CURRENT APPLICATION NUMBER: US/10/087,782  
12 <141> CURRENT FILING DATE: 2002-03-05  
14 <150> PRIOR APPLICATION NUMBER: 60/272,757  
15 <151> PRIOR FILING DATE: 2001-03-05  
17 <160> NUMBER OF SEQ ID NOS: 31  
19 <170> SOFTWARE: PatentIn Ver. 2.1

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451 Tyr Lys Thr Tyr Thr Leu Gln Asp Gly Pro Trp Ser Gln Gln Glu Arg  
452 35 40 45  
454 Asn Pro Glu Ala Pro Gly Arg Ala Ala Val Pro Pro Trp Gly Lys Tyr  
455 50 55 60  
457 Asp Ala Ala Leu Arg Thr Met Ile Pro Phe Arg Pro Lys Pro Arg Phe  
458 65 70 75 80

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464      100      105      110
466 Asp Glu Asn Thr Ile Pro Pro Leu Ser Val His Asp Ala Ser Asp Lys
467      115      120      125
469 Asn Val Gln Arg Leu His Arg Leu Trp Glu Glu Glu Val Ser Arg Arg
470      130      135      140
472 Gly Ile Glu Lys Ala Ser Val Leu Leu Val Met Leu Arg Phe Gln Arg
473 145      150      155      160
475 Thr Arg Leu Ile Phe Asp Ala Leu Leu Gly Ile Cys Phe Cys Ile Ala
476      165      170      175
478 Ser Val Leu Gly Pro Ile Leu Ile Ile Pro Lys Ile Leu Glu Tyr Ser
479      180      185      190
481 Glu Glu Gln Leu Gly Asn Val Val His Gly Val Gly Leu Cys Phe Ala
482      195      200      205
484 Leu Phe Leu Ser Glu Cys Val Lys Ser Leu Ser Phe Ser Ser Ser Trp
485      210      215      220
487 Ile Ile Asn Gln Arg Thr Ala Ile Arg Phe Arg Ala Ala Val Ser Ser
488 225      230      235      240
490 Phe Ala Phe Glu Lys Leu Ile Gln Phe Lys Ser Val Ile His Ile Thr
491      245      250      255
493 Ser Gly Glu Ala Ile Ser Phe Phe Thr Gly Asp Val Asn Tyr Leu Phe
494      260      265      270
496 Glu Gly Val Cys Tyr Gly Pro Leu Val Leu Ile Thr Cys Ala Ser Leu
497      275      280      285
499 Val Ile Cys Ser Ile Ser Ser Tyr Phe Ile Ile Gly Tyr Thr Ala Phe
500      290      295      300
502 Ile Ala Ile Leu Cys Tyr Leu Leu Val Phe Pro Leu Ala Val Phe Met
503 305      310      315      320
505 Thr Arg Met Ala Val Lys Ala Gln His His Thr Ser Glu Val Ser Asp
506      325      330      335
508 Gln Arg Ile Arg Val Thr Ser Glu Val Leu Thr Cys Ile Lys Leu Ile
509      340      345      350
511 Lys Met Tyr Thr Trp Glu Lys Pro Phe Ala Lys Ile Ile Glu Asp Leu
512      355      360      365
514 Arg Arg Lys Glu Arg Lys Leu Leu Glu Lys Cys Gly Leu Val Gln Ser
515      370      375      380
517 Leu Thr Ser Ile Thr Leu Phe Ile Ile Pro Thr Val Ala Thr Ala Val
518 385      390      395      400
520 Trp Val Leu Ile His Thr Ser Leu Lys Leu Lys Leu Thr Ala Ser Met
521      405      410      415
523 Ala Phe Ser Met Leu Ala Ser Leu Asn Leu Leu Arg Leu Ser Val Phe
524      420      425      430
526 Phe Val Pro Ile Ala Val Lys Gly Leu Thr Asn Ser Lys Ser Ala Val
527      435      440      445
529 Met Arg Phe Lys Lys Phe Phe Leu Gln Glu Ser Pro Val Phe Tyr Val
530      450      455      460
532 Gln Thr Leu Gln Asp Pro Ser Lys Ala Leu Val Phe Glu Glu Ala Thr

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## RAW SEQUENCE LISTING

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535 Leu Ser Trp Gln Gln Thr Cys Pro Gly Ile Val Asn Gly Ala Leu Glu
536          485          490          495
538 Leu Glu Arg Asn Gly His Ala Ser Glu Gly Met Thr Arg Pro Arg Asp
539          500          505          510
541 Ala Leu Gly Pro Glu Glu Glu Gly Asn Ser Leu Gly Pro Glu Leu His
542          515          520          525
544 Lys Ile Asn Leu Val Val Ser Lys Gly Met Met Leu Gly Val Cys Gly
545          530          535          540
547 Asn Thr Gly Ser Gly Lys Ser Ser Leu Leu Ser Ala Ile Leu Glu Glu
548 545          550          555          560
550 Met His Leu Leu Glu Gly Ser Val Gly Val Gln Gly Ser Leu Ala Tyr
551          565          570          575
553 Val Pro Gln Gln Ala Trp Ile Val Ser Gly Asn Ile Arg Glu Asn Ile
554          580          585          590
556 Leu Met Gly Gly Ala Tyr Asp Lys Ala Arg Tyr Leu Gln Val Leu His
557          595          600          605
559 Cys Cys Ser Leu Asn Arg Asp Leu Glu Leu Leu Pro Phe Gly Asp Met
560          610          615          620
562 Thr Glu Ile Gly Glu Arg Gly Leu Asn Leu Ser Gly Gly Gln Lys Gln
563 625          630          635          640
565 Arg Ile Ser Leu Ala Arg Ala Val Tyr Ser Asp Arg Gln Ile Tyr Leu
566          645          650          655
568 Leu Asp Asp Pro Leu Ser Ala Val Asp Ala His Val Gly Lys His Ile
569          660          665          670
571 Phe Glu Glu Cys Ile Lys Lys Thr Leu Arg Gly Lys Thr Val Val Leu
572          675          680          685
574 Val Thr His Gln Leu Gln Tyr Leu Glu Phe Cys Gly Gln Ile Ile Leu
575          690          695          700
577 Leu Glu Asn Gly Lys Ile Cys Glu Asn Gly Thr His Ser Glu Leu Met
578 705          710          715          720
580 Gln Lys Lys Gly Lys Tyr Ala Gln Leu Ile Gln Lys Met His Lys Glu
581          725          730          735
583 Ala Thr Ser Asp Met Leu Gln Asp Thr Ala Lys Ile Ala Glu Lys Pro
584          740          745          750
586 Lys Val Glu Ser Gln Ala Leu Ala Thr Ser Leu Glu Glu Ser Leu Asn
587          755          760          765
589 Gly Asn Ala Val Pro Glu His Gln Leu Thr Gln Glu Glu Met Glu
590          770          775          780
592 Glu Gly Ser Leu Ser Trp Arg Val Tyr His His Tyr Ile Gln Ala Ala
593 785          790          795          800
595 Gly Gly Tyr Met Val Ser Cys Ile Ile Phe Phe Phe Val Val Leu Ile
596          805          810          815
598 Val Phe Leu Thr Ile Phe Ser Phe Trp Trp Leu Ser Tyr Trp Leu Glu
599          820          825          830
601 Gln Gly Ser Gly Thr Asn Ser Ser Arg Glu Ser Asn Gly Thr Met Ala
602          835          840          845
604 Asp Leu Gly Asn Ile Ala Asp Asn Pro Gln Leu Ser Phe Tyr Gln Leu
605          850          855          860

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610 Ser Gly Ile Phe Thr Lys Val Thr Arg Lys Ala Ser Thr Ala Leu His
611      885      890      895
613 Asn Lys Leu Phe Asn Lys Val Phe Arg Cys Pro Met Ser Phe Phe Asp
614      900      905      910
616 Thr Ile Pro Ile Gly Arg Leu Leu Asn Cys Phe Ala Gly Asp Leu Glu
617      915      920      925
619 Gln Leu Asp Gln Leu Leu Pro Ile Phe Ser Glu Gln Phe Leu Val Leu
620      930      935      940
622 Ser Leu Met Val Ile Ala Val Leu Leu Ile Val Ser Val Leu Ser Pro
623 945      950      955      960
625 Tyr Ile Leu Leu Met Gly Ala Ile Ile Met Val Ile Cys Phe Ile Tyr
626      965      970      975
628 Tyr Met Met Phe Lys Lys Ala Ile Gly Val Phe Lys Arg Leu Glu Asn
629      980      985      990
631 Tyr Ser Arg Ser Pro Leu Phe Ser His Ile Leu Asn Ser Leu Gln Gly
632      995      1000      1005
634 Leu Ser Ser Ile His Val Tyr Gly Lys Thr Glu Asp Phe Ile Ser Gln
635      1010      1015      1020
637 Phe Lys Arg Leu Thr Asp Ala Gln Asn Asn Tyr Leu Leu Leu Phe Leu
638 1025      1030      1035      1040
640 Ser Ser Thr Arg Trp Met Ala Leu Arg Leu Glu Ile Met Thr Asn Leu
641      1045      1050      1055
643 Val Thr Leu Ala Val Ala Leu Phe Val Ala Phe Gly Ile Ser Ser Thr
644      1060      1065      1070
646 Pro Tyr Ser Phe Lys Val Met Ala Val Asn Ile Val Leu Gln Leu Ala
647      1075      1080      1085
649 Ser Ser Phe Gln Ala Thr Ala Arg Ile Gly Leu Glu Thr Glu Ala Gln
650      1090      1095      1100
652 Phe Thr Ala Val Glu Arg Ile Leu Gln Tyr Met Lys Met Cys Val Ser
653 1105      1110      1115      1120
655 Glu Ala Pro Leu His Met Glu Gly Thr Ser Cys Pro Gln Gly Trp Pro
656      1125      1130      1135
658 Gln His Gly Glu Ile Ile Phe Gln Asp Tyr His Met Lys Tyr Arg Asp
659      1140      1145      1150
661 Asn Thr Pro Thr Val Leu His Gly Ile Asn Leu Thr Ile Arg Gly His
662      1155      1160      1165
664 Glu Val Val Gly Ile Val Gly Arg Thr Gly Ser Gly Lys Ser Ser Leu
665      1170      1175      1180
667 Gly Met Ala Leu Phe Arg Leu Val Glu Pro Met Ala Gly Arg Ile Leu
668 1185      1190      1195      1200
670 Ile Asp Gly Val Asp Ile Cys Ser Ile Gly Leu Glu Asp Leu Arg Ser
671      1205      1210      1215
673 Lys Leu Ser Val Ile Pro Gln Asp Pro Val Leu Leu Ser Gly Thr Ile
674      1220      1225      1230
676 Arg Phe Asn Leu Asp Pro Phe Asp Arg His Thr Asp Gln Gln Ile Trp
677      1235      1240      1245
679 Asp Ala Leu Glu Arg Thr Phe Leu Thr Lys Ala Ile Ser Lys Phe Pro

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683 1265                      1270                      1275                      1280  
685 Gly Glu Arg Gln Leu Leu Cys Ile Ala Arg Ala Val Leu Arg Asn Ser  
686                      1285                      1290                      1295  
688 Lys Ile Ile Leu Ile Asp Glu Ala Thr Ala Ser Ile Asp Met Glu Thr  
689                      1300                      1305                      1310  
691 Asp Thr Leu Ile Gln Arg Thr Ile Arg Glu Ala Phe Gln Gly Cys Thr  
692                      1315                      1320                      1325  
694 Val Leu Val Ile Ala His Arg Val Thr Thr Val Leu Asn Cys Asp His  
695                      1330                      1335                      1340  
697 Ile Leu Val Met Gly Asn Gly Lys Val Val Glu Phe Asp Arg Pro Glu  
698 1345                      1350                      1355                      1360  
700 Val Leu Arg Lys Lys Pro Gly Ser Leu Phe Ala Ala Leu Met Ala Thr  
701                      1365                      1370                      1375  
703 Ala Thr Ser Ser Leu Arg  
704                      1380

E--&gt;

710

(1)

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## VERIFICATION SUMMARY

PATENT APPLICATION: US/10/087,782

DATE: 03/20/2002

TIME: 16:25:10

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L:710 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:31